1	CAAACTTGGT	GGCAACTTGC	CTCCCGGTGC	GGGCGTCTCT	CCCCCACCGT
51	CTCAA C <u>ATG</u> C	TTAGGGGTCC	GGGGCCCGGG	CTGCTGCTGC	TGGCCGTCCA
101	GTGCCTGGGG	ACAGCGGTGC	CCTCCACGGG	AGCCTCGAAG	AGCAAGAGGC
151	AGGCTCAGCA	AATGGTTCAG	CCCCAGTCCC	CGGTGGCTGT	CAGTCAAAGC
201	AAGCCCGGTT	GTTATGACAA	TGGAAAACAC	TATCAGATAA	ATCAACAGTG
251	GGAGCGGACC	TACCTAGGCA	ATGCGTTGGT	TTGTACTTGT	TATGGAGGAA
301	GCCGAGGTTT	TAACTGCGAG	AGTAAACCTG	AAGCTGAAGA	GACTTGCTTT
351	GACAAGTACA	CTGGGAACAC	TTACCGAGTG	GGTGACACTT	ATGAGCGTCC
401	TAAAGACTCC	ATGATCTGGG	ACTGTACCTG	CATCGGGGCT	GGGCGAGGGA
451	GAATAAGCTG	TACCATCGCA	AACCGCTGCC	ATGAAGGGGG	TCAGTCCTAC
501	AAGATTGGTG	ACACCTGGAG	GAGACCACAT	GAGACTGGTG	GTTACATGTT
551	AGAGTGTGTG	TGTCTTGGTA	ATGGAAAAGG	AGAATGGACC	TGCAAGCCCA
601	TAGCTGAGAA	GTGTTTTGAT	CATGCTGCTG	GGACTTCCTA	TGTGGTCGGA
651	GAAACGTGGG	AGAAGCCCTA	CCAAGGCTGG	ATGATGGTAG	ATTGTACTTG
701	CCTGGGAGAA	GGCAGCGGAC	GCATCACTTG	CACTTCTAGA	AATAGATGCA
751	ACGATCAGGA	CACAAGGACA	TCCTATAGAA	TTGGAGACAC	CTGGAGCAAG
801	AAGGATAATC	GAGGAAACCT	GCTCCAGTGC	ATCTGCACAG	GCAACGGCCG
851	AGGAGAGTGG	AAGTGTGAGA	GGCACACCTC	TGTGCAGACC	ACATCGAGCG
901	GATCTGGCCC	CTTCACCGAT	GTTCGTGCAG	CTGTTTACCA	ACCGCAGCCT
951	CACCCCCAGC	CTCCTCCCTA	TGGCCACTGT	GTCACAGACA	GTGGTGTGGT
1001	CTACTCTGTG	GGGATGCAGT	GGCTGAAGAC	ACAAGGAAAT	AAGCAAATGC
1051	TTTGCACGTG	CCTGGGCAAC	GGAGTCAGCT	GCCAAGAGAC	AGCTGTAACC

Fig. 1 (part 1)

1101	CAGACTTACG GTGGCAACTC AAATGGAGAG CCATGTGTCT TACCATTCAC
1151	CTACAACGAC AGGACGGACA GCACAACTTC GAATTATGAG CAGGACCAGA
1201	AATACTCTTT CTGCACAGAC CACACTGTTT TGGTTCAGAC TCGAGGAGGA
1251	AATTCCAATG GTGCCTTGTG CCACTTCCCC TTCCTATACA ACAACCACAA
1301	TTACACTGAT TGCACTTCTG AGGGCAGAAG AGACAACATG AAGTGGTGTG
1351	GGACCACACA GAACTATGAT GCCGACCAGA AGTTTGGGTT CTGCCCCATG
1401	GCTGCCCACG AGGAAATCTG CACAACCAAT GAAGGGGTCA TGTACCGCAT
1451	TGGAGATCAG TGGGATAAGC AGCATGACAT GGGTCACATG ATGAGGTGCA
1501	CGTGTGTTGG GAATGGTCGT GGGGAATGGA CATGCATTGC CTACTCGCAG
1551	CTTCGAGATC AGTGCATTGT TGATGACATC ACTTACAATG TGAACGACAC
1601	ATTCCACAAG CGTCATGAAG AGGGGCACAT GCTGAACTGT ACATGCTTCG
1651	GTCAGGGTCG GGGCAGGTGG AAGTGTGATC CCGTCGACCA ATGCCAGGAT $$
1701	TCAGAGACTG GGACGTTTTA TCAAATTGGA GATTCATGGG AGAAGTATGT
1751	GCATGGTGTC AGATACCAGT GCTACTGCTA TGGCCGTGGC ATTGGGGAGT
1801	GGCATTGCCA ACCTTTACAG ACCTATCCAA GCTCAAGTGG TCCTGTCGAA
1851	GTATTTATCA CTGAGACTCC GAGTCAGCCC AACTCCCACC CCATCCAGTG
1901	GAATGCACCA CAGCCATCTC ACATTTCCAA GTACATTCTC AGGTGGAGAC
1951	CTGTGAGTAT CCCACCCAGA AACCTTGGAT ACTGAGTCTC CTAATCTTAT
2001	CAATTCTGAT GGTTTCTTTT TTTCCCAGCT TTTGAGCCAA CAACTCTGAT
2051	TAACTATICC TATAGCATTT ACTATATITG TITAGTGAAC AAACAATATG
2101	TGGTCAATTA AATTGACTTG TAGACTGAAA AAAAAAAAA AAAAAAA

Fig. 1 (part 2)

wan .	10	20	30	40	50	60
PMSF-1α	NLVATCLPVRASLPH	RLNMLRGPGP	GLLLLAVQCI	GTAVPSTGA	SKSKRQAQQI	WOPOSP
fibronectin	NLVATCLPVRASLPH	RLNMLRGPGP	GLLLLAVQCI	GTAVPSTGA:		MVODOGD
			10	20	30	40
	70	80	90	100	110	120
PMSF-1α	VAVSQSKPGCYDNGK	HYQINQQWER	TYLGNALVCT	CAGGEBURN	TECEDES ED	
fibronectin	111111111111111	111111111	11111:1111	111111111		HILLIA
	VAVSQSKPGCYDNGK 50	EO COMPAN	70	CYGGSRGFNO 80	CESKPEAEE 90	ICFDKYT 100
	***					100
p MSF-1α	130 GNTYRVGDTYERPKD	140	150	160	170	180
	11111111111111111	1111111111	11111111111	1111111111		
fibronectin	GNIIRVGDIIERPKD	SMINDCTCIG.	AGRGRISCTI	ANRCHEGGQ	SYKIGDTWR	RPHETGG
	110	120	130	140	150	160
	190	200	210	220	230	240
pMSF-1α	YMLECVCLGNGKGEW	TCKPIAEKCF	DHAAGTSYVV	GETWEKPYQ	WMMVDCTC	LGEGSGR
fibronectin	YMLECVCLGNGKGEW	TCKPIAEKCE	HAAGTSYVV			[[]]
	170	180	190	200	210	220
	250	260	270	280	290	300
pMSF-1α	ITCTSRNRCNDQDTR	TSYRIGDTWS	KKDNRGNLLC	CICTGNGRG	WKCERHTS	COTTECC
fibronectio			1111111111	111111111		HILLER
2202011600111	230		ккомкомыц 250	CICTGNGRG	EWKCERHTS	VQTTSSG 280
						200
p MSF-1α	310 SGPFTDVRAAVYQPQ	320	330	340	350	360
•	1111111111111111	1111111111	1111111111	THILLIAM		LILLIA
fibronectin	SGPFTDVRAAVYQPQ	PHPQPPPYGH	CVTDSGVVYS	VGMQWLKTQ	GNKQMLCTC:	LGNGVSC
	290	300	310	320	330	340
	370	380		39		00
PMSF-1α	QETAVTQTYGGNSNG	EPCVLPFTYN	DRT			
fibronectin	QETAVTQTYGGNSNG	EPCVLPFTYN	: GRTFYSCTTE	GRODGHT.WC	STISNABOD	OKAGECA
	350	360	370	380	390	400
	410 420	430	440) 45		60
pMSF-1α	DHTVLVOTRGGNSNG	ALCHEPFLYN	NHNYTOCTS	CREDIMMENO	Cumorino d	ovranan
fibronection		1111111111	11111111			
	DHTVLVQTQGGNSNG 410	ALCHEPFLYN	NHNYTDCTSI 430	GRRDNMKWC 440	GTTQNYDAD 450	QKFGFCP
					130	460

Fig. 2 (part 1)

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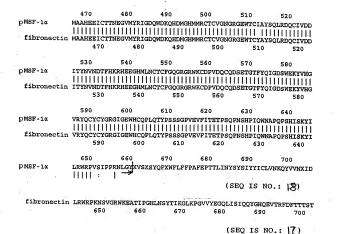


Fig. 2 (part 2)

NUMATCLEPWRASLEHRLN **MALRGEOGRILLLAVOCLGTAVPSTGASKSKR* **ACACOMYOFOGSPVANSOGKRG* **ACACOMYOFOGSPVANSOGKRG* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGSRGFNCESKFEARER* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGSRGFNCESKFEARER* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGSRGFNCESKFEARER* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGSRGFNCESKFEARER* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGSRGFNCESKFEARER* **CYDNOGHYOLOGYMERTYLONALVCTCYGGGRGFNCESKFEARER* **SEQ ID NO: 15] I Fibrin Heparin Hep					REPLA	CEME	ENT SHE	EET				
SEQ ID NO: Sequence Type Binding Site (SEQ ID NO: 13] 5' untranslated region (SEQ ID NO: 14] Signal (SEQ ID NO: 15] II (SEQ ID NO: 16] I (SEQ ID NO: 18] I (SEQ ID NO: 18] I (SEQ ID NO: 17) I (SEQ ID NO: 19) I (SEQ ID NO: 19) I (SEQ ID NO: 19) I (SEQ ID NO: 20) II (SEQ ID NO: 28) II (SEQ ID NO: 23) I	*VS*SYQF*WELFEPAFEPTTLINYSYSIYYICLVNKQYVVN*IDL*TEKKKKKI	633VSIPPRNIGY	594SGEVEVFITETPSQENSHPIQWNAPQPSHISKYILRWRP	45CTTNEGVNYRIGDQWDKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQ 30CLYDDITYNNUDTHKRHEEGHMLNCTCFGQGRGRWKCDFVDQ 545CQDSETGTFYQIGDSWEKYVHGVRYQCYCCYGRGIGEWHCQPLQTYPSS	349TAVTQTYGGNSNGEECVLFETYNDRTDSTTSNYEQDQKYSFCTDH 350TVLVQTRGGNSNGALCHFFFLYNNHNYTDCTSEGRRDNAKWCGTT QNYDADQKFGFCPMAHEEI	305CVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQE	HDY444QH4QQHVAAAAATTTSSSSSTTTSVSTH ^{rz}	18%CFDHAAGTSYVVGETWEKEYQGWMMVDCTCLGEGSGRITGTSRNR 23%CNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCER	SCYDNOKHYOINOOMERTYLGNALVCTCYGGSRGFNCESKFEAEET STGFDKYTGNTYRVGDTYERFKDSHIMDCYCIGAGRGRISCTIANR 14CHEGGGSYKTGDTWRREPERFKDSHIMDCYCTTAGAGAGATSCTIANR	¹ MLRGFGFGILILAVQCLGTAVESTGASKSKR ²² QAQQWQFQSFVAVSQSKFG	NIVATCLEVRASLEHRLN	
ID NO: Sequence Type Binding Site ID NO; 13] 5' untranslated region ID NO:14] Signal ID NO:15] NH2-terminal segment ID NO:36] I Fibrin ID NO:38] I Fibrin ID NO:39] I Heparin ID NO:40] I Saureus ID NO:19] Connecting Strand ID NO:19] I Gelatin ID NO:20] II Gelatin ID NO:21] I Gelatin ID NO:22] I I I NO:23] I I I NO:23] I I NO:23] I I NO:24] III NO:24] III NO:25] III NO:23] I I NO:23] I I NO:23] I I NO:23] I I NO:23] I NO:23] I I NO:23] I NO:	([SEQ	[SEQ	[SEQ	0as] 0as] 0as]	ðas] ðas]	Oas]	OES]	(SEC)	038] 038]	Oas]	[SEQ	SEQ
Sequence Type Binding Site No; 13] 5' untranslated region No:14] Signal No:15] I No:16] I No:39] I No:39] I No:39] I No:39] I No:40] I N	ID N	ID N	ID N	H H H	ID N	ID N	ID N	###	4 4 4	1 H	Ħ	I V
Sequence Type Binding Site Signal Signal Fibrin I Fibrin Gelatin I Fibrin Gelatin I Fibrin Gelatin Gelatin	0: 2			000	0 0 2 2	0: 1	10:18	40:40 40:17		NO: 14	No,	ņ
Sequence Type Binding Site 5' untranslated region Signal NH2-terminal segment I I I Connecting strand I I I I I I I I I I I I I I I I I I I	9-33]			3] 2]	8]	9]	_		9 9	.5]	ω	
Binding Site region ment Fibrin Heparin S. aureus Gelatin Gelatin	3' untranslated r	Unique Sequence	III	ннн	HH	н	Connecting strang	нн		Signal NH2-terminal seg	.5' untranslated	Sequence Type
	region				Gelatin		ρ.	S. aureus	Fibrin	ment	region	Binding Site

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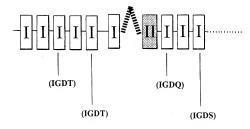


Fig. 4



Fig. 5